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OM protein - protein search, using sw model

Run on: April 22, 2004, 13:50:23 ; Search time 18 Seconds
(without alignments)

1423.251 Million cell updates/sec

Title: US-09-978-188a-7
Perfect score: 2527
Sequence: 1 MYKFPALHWPLRFLVPL.....TDMPTTEVDIVRENE 492

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2527	100.0	492	1 ANKH HUMAN	Q9HCJ1 homo sapien
2	2502	99.0	492	1 ANKH MOUSE	Q9JH22 mus musculu
3	2489	98.5	492	1 ANKH RAT	P58366 rattus norv
4	2317	91.7	492	1 ANKH XENLA	P58367 xenopus lae
5	2158.5	85.4	501	1 ANKH BRAPE	P58368 brachydanio
6	1528.5	60.5	355	1 ANKH TETNG	P58369 terradon n
7	114	4.5	416	1 LACY KLEOX	P18817 klebsiella
8	113.5	4.5	556	1 NUDM PODAN	P15878 podospora a
9	111	4.4	622	1 COX1 BACSU	P24010 bacillus su
10	109.5	4.3	610	1 PTXA ARATH	P46031 arabidopsis
11	107	4.2	422	1 EXMT BACSU	Q34456 bacillus su
12	107	4.2	533	1 LAR2 RAT	Q9WYR6 rattus norv
13	106	4.2	334	1 LAR2 METUA	Q58578 methanococc
14	105	4.2	401	1 LSG1 HAEIN	P71399 haemophilus
15	105	4.2	476	1 HPI1 METAC	Q81723 haemophilus
16	103.5	4.1	398	1 BCR HAEIN	P45123 haemophilus
17	103	4.1	417	1 LACY ECOLI	P02920 escherichia
18	102.5	4.1	446	1 CITR SALTU	P31604 salmonella
19	102.5	4.1	531	1 LAR2 MOUSE	Q9GQW9 mus musculu
20	102.5	4.1	533	1 MVIN RHITR	Q05467 rhizobium t
21	102.5	4.1	641	1 NUSM ALLMA	P30365 allomyces m
22	101.5	4.0	446	1 CITR SALDU	P31603 salmonella
23	100	4.0	982	1 YS96 CAEEL	Q09965 caenorhabdi
24	99	3.9	385	1 Y421 METTH	Q26521 methanobact
25	99	3.9	535	1 LAR2 HUMAN	Q9UN15 homo sapien
26	98.5	3.9	583	1 NUDM NEUCR	Q35140 neurospora
27	98.5	3.9	946	1 YBTE YEAST	P38250 saccharomyc
28	98	3.9	480	1 YEH4 YEAST	P39981 saccharomyc
29	98	3.9	532	1 YAHM BACST	P37555 bacillus su
30	97.5	3.9	346	1 FMR1 PONPY	P79335 pongo pygma
31	97.5	3.9	3803	1 TYCB DROME	Q81807 drosofila
32	97	3.8	402	1 YTCB BACSU	P37482 bacillus su
33	96.5	3.8	346	1 FMR1 GORGO	P79176 gorilla gor

34	95.5	3.8	416	1 LACY CITR	P47234 citrobacter
35	95.5	3.8	483	1 NORM_VIBVU	Q8d98 vibrio vuln
36	95	3.8	457	1 NORM_ECO57	P58164 escherichia
37	95	3.8	459	1 NU4M BALPH	P24975 balaeonopter
38	95	3.8	460	1 NU4M ASTPE	P11992 asterina pe
39	95	3.8	464	1 NORM_HAEIN	P45272 haemophilus
40	95	3.8	501	1 LYX1 CORGL	P35865 corynebacte
41	95	3.8	511	1 ALG8 DROME	Q9W308 drosofila
42	95	3.8	654	1 NUDM RHIST	P50367 rhizopus st
43	94.5	3.7	507	1 TT12 ARATH	Q91Y13 arabidopsis
44	94.5	3.7	518	1 SP58 BACSU	Q00758 bacillus su
45	94	3.7	421	1 VG2_EPRKE	P03660 bacterioph

ALIGNMENTS

RESULT 1	ANKH HUMAN	STANDARD;	PRT;	492 AA.
AC	Q9HCJ1; Q9NCW2;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Progressive ankylosis protein homolog (ANK).			
GN	ANKH OR KIAA1581.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OK	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20355194; PubMed=10894769;			
RA	Ho A.M., Johnson M.D., Kingsley D.M.;			
RT	"Role of the mouse ank gene in control of tissue calcification and			
RT	arthritis.";			
RL	Science 289:265-270(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=20450683; PubMed=10997877;			
RA	Nagase T., Kikuno R., Nakayama M., Hirose M., Ohara O.;			
RT	"Prediction of the coding sequences of unidentified human genes.			
RT	XVII. The complete sequences of 100 new cDNA clones from brain which			
RT	code for large proteins in vitro.";			
RL	Lab. Res. 7:273-281(2000).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Ovary;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Klausner R.D., Collins P.S., Wagner L., Shemen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Cavaletto T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Bouffard G.G.,			
RA	Raha S.S., Iqbal N.A., Peters G.J., Abramson R.D., Gunaratne P.H.,			
RA	Boeck S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Wuzny D.M., Sodergren E.U., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield J.S.N., Krzyzinski M.T., Skalska U., Smalins D.E.,			
RA	Schneier A., Schein J.E., Jones S.J.W., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length			
RT	human and mouse cDNA sequences.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16839-16903(2002).			
RN	[4]			
RP	VARIANTS CMDJ SER-375 DEL; PHE-376 DEL AND ALA-380 INS.			
RX	MEDLINE=21313103; PubMed=11326338;			

RA Reichenberger E., Tiziani V., Matanabe S., Park L., Ueki Y.,
 RA Santanna C., Baur S.T., Shiang R., Grange D.K., Beighton P.,
 RA Gardner J., Hamersma H., Sellars S., Ramesar R., Lital A.C.,
 RA Sommer A., Raposo do Amaral C.M., Gorlin R.J., Mulliken J.B.,
 RA Olsen B.R.;
 RT "Autosomal dominant craniofacial dysplasia is caused by mutations
 in the transmembrane protein ANK-";
 RL Am. J. Hum. Genet. 68:1321-1326(2001).
 RN [5]
 RP VARIANTS CMDJ ARG-292; ARG-331; SER-375 DEL; PHE-377 DEL; ALA-380 INS
 RP AND ARG-389.
 RX MEDLINE=11225282; PubMed=11326272;
 RA Nienberg P., Thiele H., Chandler D., Hoehe W., Cunningham M.L.,
 RA Bitter H., Leschik G., Uhlmann K., Mischung C., Harrop K.,
 RA Goldblatt J., Borochowitz Z.U., Kotzot D., Westermann F., Mundlos S.,
 RA Braun H.-S., Laing N., Tinschert S.;
 RT "Heterozygous mutations in ANKH, the human ortholog of the mouse
 progressive ankylosis gene, result in craniofacial dysplasia";
 RL Nat. Genet. 28:37-41(2001).
 CC -1- FUNCTION: Regulates intra- and extracellular levels of inorganic
 phosphate (P_{ii}), probably functioning as P_{ii} transporter.
 CC SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- TISSUE SPECIFICITY: Found in osteoblasts from mandibular bone and
 from iliac bone; not detected in osteoclastic cells.
 CC -1- DISEASE: Defects in ANKH are the cause of craniofacial dysplasia
 dysplasia Jackson type (CMDJ) [MIM:123000]. CMDJ is a rare
 autosomal dominant skeletal disorder characterized by abnormal
 bone formation and mineralization in membranous as well as
 endochondral bones. Progressive thickening of the bones can cause
 narrowing of cranial foramina and can lead to severe visual and
 neurological impairment, such as facial palsy and deafness.
 CC -1- SIMILARITY: BELONGS TO THE ANKH FAMILY.
 CC -----
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 DR EMBL; AF274753; AAF88039.1; -;
 DR EMBL; AB046801; BAB13407.1; ALT_INIT.
 DR EMBL; BC009835; AAH09835.1; -;
 DR EMBL; BC014526; AAH14526.1; -;
 DR Genew; HGNC:15492; ANKH.
 DR MIM; 605145; -;
 DR MIM; 123000; -;
 DR GO; GO:0016021; C:integral to membrane; IDA.
 DR GO; GO:0019667; C:outer membrane; TAS.
 DR GO; GO:0030504; F:inorganic diphosphate transporter activity; IDA.
 DR GO; GO:0005315; F:inorganic phosphate transporter activity; IDA.
 DR GO; GO:0007666; P:locomotory behavior; NAS.
 DR GO; GO:0030500; P:regulation of bone mineralization; TAS.
 DR GO; GO:0001501; P:skeletal development; NAS.
 KM Transport; Phosphate transport; Transmembrane; Disease mutation;
 KM Deafness.
 FT DOMAIN 1 85 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 86 106 POTENTIAL.
 FT DOMAIN 107 131 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 132 152 POTENTIAL.
 FT DOMAIN 153 158 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 159 179 POTENTIAL.
 FT DOMAIN 180 189 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 190 210 POTENTIAL.
 FT DOMAIN 211 326 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 327 347 POTENTIAL.
 FT DOMAIN 348 350 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 351 371 POTENTIAL.
 FT TRANSSEM 372 403 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 404 426 POTENTIAL.
 FT TRANSSEM 427 429 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 430 452 POTENTIAL.

FT DOMAIN 453 492 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 493 522 W -> R (in CMDJ).
 FT VARIANT 292 292 /FTID=VAR 012192.
 FT VARIANT 331 331 C -> R (in CMDJ).
 FT VARIANT 331 331 /FTID=VAR 012193.
 FT VARIANT 375 375 Missing (in CMDJ).
 FT VARIANT 376 376 /FTID=VAR 012194.
 FT VARIANT 376 376 Missing (in CMDJ).
 FT VARIANT 377 377 /FTID=VAR 012195.
 FT VARIANT 377 377 Missing (in CMDJ).
 FT VARIANT 380 380 /FTID=VAR 012196.
 FT VARIANT 380 380 P -> PA (in CMDJ).
 FT VARIANT 389 389 /FTID=VAR 012197.
 FT VARIANT 389 389 G -> R (in CMDJ).
 FT CONFLICT 78 78 /FTID=VAR 012198.
 FT SEQUENCE 492 AA; 54240 MW; 44BE83089BDEC6B CRC64;
 SQ
 Query Match 100.0%; Score 2527; DB 1; Length 492;
 Best Local Similarity 100.0%; Pred. No. 7, 8e-195;
 Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MYKFPALTYHWPILRFLVPLGINTINAIIDFGEQALNNGIAVYEDAVEMTASVGLAYSLMK 60
 1 MYKFPALTYHWPILRFLVPLGINTINAIIDFGEQALNNGIAVYEDAVEMTASVGLAYSLMK 60
 DB 61 FTGSPMDPKNVGLVFNVSKRDRTKAVLCMVVAGALAAVPHLLAYSDGIYINKLHHY 120
 61 FTGSPMDPKNVGLVFNVSKRDRTKAVLCMVVAGALAAVPHLLAYSDGIYINKLHHY 120
 DB 121 DESVGSKTRRAPFLYLAFFPMAMANTHAGILKHKYSLVGCASISDVIAQVFAVILL 180
 121 DESVGSKTRRAPFLYLAFFPMAMANTHAGILKHKYSLVGCASISDVIAQVFAVILL 180
 DB 121 DESVGSKTRRAPFLYLAFFPMAMANTHAGILKHKYSLVGCASISDVIAQVFAVILL 180
 121 DESVGSKTRRAPFLYLAFFPMAMANTHAGILKHKYSLVGCASISDVIAQVFAVILL 180
 QY 181 HSHLECRREPLIPILSLYMGALVRCYLLCLGYKNIHDIIPDRSGELGADATIRKQLSF 240
 181 HSHLECRREPLIPILSLYMGALVRCYLLCLGYKNIHDIIPDRSGELGADATIRKQLSF 240
 DB 181 HSHLECRREPLIPILSLYMGALVRCYLLCLGYKNIHDIIPDRSGELGADATIRKQLSF 240
 181 HSHLECRREPLIPILSLYMGALVRCYLLCLGYKNIHDIIPDRSGELGADATIRKQLSF 240
 QY 241 WMLALILNORISRIIVLVFVSRDLAGSSAAEVAAILATATPVGMPPYGMWLTETRAVY 300
 241 WMLALILNORISRIIVLVFVSRDLAGSSAAEVAAILATATPVGMPPYGMWLTETRAVY 300
 DB 241 WMLALILNORISRIIVLVFVSRDLAGSSAAEVAAILATATPVGMPPYGMWLTETRAVY 300
 241 WMLALILNORISRIIVLVFVSRDLAGSSAAEVAAILATATPVGMPPYGMWLTETRAVY 300
 QY 301 PAFDKNPNKLVSTENTVTAHIKKFTFCVALSTLTCFVWPTNVSEKILIDIIIGVD 360
 301 PAFDKNPNKLVSTENTVTAHIKKFTFCVALSTLTCFVWPTNVSEKILIDIIIGVD 360
 DB 301 PAFDKNPNKLVSTENTVTAHIKKFTFCVALSTLTCFVWPTNVSEKILIDIIIGVD 360
 301 PAFDKNPNKLVSTENTVTAHIKKFTFCVALSTLTCFVWPTNVSEKILIDIIIGVD 360
 QY 361 PAFPAELCVPLRIFFSPFPVPTVRAHLTGMLTKTFTVLABSVALRIIVLISLVLPY 420
 361 PAFPAELCVPLRIFFSPFPVPTVRAHLTGMLTKTFTVLABSVALRIIVLISLVLPY 420
 DB 361 PAFPAELCVPLRIFFSPFPVPTVRAHLTGMLTKTFTVLABSVALRIIVLISLVLPY 420
 361 PAFPAELCVPLRIFFSPFPVPTVRAHLTGMLTKTFTVLABSVALRIIVLISLVLPY 420
 QY 421 LGVHGAATLGVSLAGVGSSTVVAIAACVVRKOKKKNENESATGEDSAMTDMPTTEE 480
 421 LGVHGAATLGVSLAGVGSSTVVAIAACVVRKOKKKNENESATGEDSAMTDMPTTEE 480
 DB 421 LGVHGAATLGVSLAGVGSSTVVAIAACVVRKOKKKNENESATGEDSAMTDMPTTEE 480
 421 LGVHGAATLGVSLAGVGSSTVVAIAACVVRKOKKKNENESATGEDSAMTDMPTTEE 480
 QY 481 VTDIVEMREENE 492
 481 VTDIVEMREENE 492
 DB 481 VTDIVEMREENE 492
 481 VTDIVEMREENE 492
 RESULT 2
 ANKH MOUSE STANDARD; PRT; 492 AA.
 ID ANKH MOUSE STANDARD; PRT; 492 AA.
 AC O9THZ2; O35138; O35139;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Progressive ankylosis protein (Fn54 protein).
 OS ANKH OR ANK.
 GN Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

[illegible]

QY 721 CAAGACATTCAGCAATCATCCTGACAGAAAGTGGCCCGGAGCTGGGGGAGATGCAAC 780
DB 800 CAGAAACATTCACACATCATCTCCGACAGAAAGTGGCCCGGAGCTGGGGGAGATGCAAC 859
QY 781 AATAAGAAAGATGTGAGCTTCTGGTGGCTTTGGCTCTAATTTGCGCAACAGAGAAAT 840
DB 860 AATAAGAAAGATGTGAGCTTCTGGTGGCTTTGGCTCTAATTTGCGCAACAGAGAAAT 919
QY 841 CAGTGGCTTATTTGCAACCTCTTTTGTTCGGGACCTTGGTGGCAATTCGAGCCAC 900
DB 920 CAGTGGCTTATTTGCAACCTCTTTTGTTCGGGACCTTGGTGGCAATTCGAGCCAC 979
QY 901 AGAGGAGTGGCGGATTTTGAACGCCAATATCCCTGGGTGACATGCCAATGCGCTGTT 960
DB 980 AGAGGAGTGGCGGATTTTGAACGCCAATATCCCTGGGTGACATGCCAATGCGCTGTT 1039
QY 961 GACGAAATCCGTCCTGTATCTGCTTTGCAAGAAATPACCCGACAAACAACTGAT 1020
DB 1040 GACGAAATCCGTCCTGTATCTGCTTTGCAAGAAATPACCCGACAAACAACTGAT 1099
QY 1021 GAGCAGAGCAACACAGTCAAGGACCCACATCAAGAAATTCACCTTCTGTCATGAC 1080
DB 1100 GAGCAGAGCAACACAGTCAAGGACCCACATCAAGAAATTCACCTTCTGTCATGAC 1159
QY 1081 TCTGTACATCAAGCTGTTTGGATTTTGGACACCCAAAGTGTCTGAGAAATCTT 1140
DB 1160 TCTGTACATCAAGCTGTTTGGATTTTGGACACCCAAAGTGTCTGAGAAATCTT 1219
QY 1141 GATAGACATCATCGAGTGAATTTGCTTGGCAACTCTGTTGTTGCTTGGCGGAT 1200
DB 1220 GATAGACATCATCGAGTGAATTTGCTTGGCAACTCTGTTGTTGCTTGGCGGAT 1279
QY 1201 CTCTCTCTTTTCCAGTTCAGTCAAGTGAAGGCGCATCTCAACCGGATGCTGATGAC 1260
DB 1280 CTCTCTCTTTTCCAGTTCAGTCAAGTGAAGGCGCATCTCAACCGGATGCTGATGAC 1339
QY 1261 ACTGAAGAAACCTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1340 ACTGAAGAAACCTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1399
QY 1321 CAGCCTCTGTCCTTACCTTACCTGAGGAGTGAACAGTGGACCTGGGCGTGGGCTCCCT 1380
DB 1400 CAGCCTCTGTCCTTACCTTACCTGAGGAGTGAACAGTGGACCTGGGCGTGGGCTCCCT 1459
QY 1381 CCTGGGCGGCTTTGGTGAAGATTCACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
DB 1460 CCTGGGCGGCTTTGGTGAAGATTCACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1519
QY 1441 GAAGCAGAAAGAAAGATGAGATGAGTGGCCACAGAGGGGGAAGATCTTGCATGAC 1500
DB 1520 GAAGCAGAAAGAAAGATGAGATGAGTGGCCACAGAGGGGGAAGATCTTGCATGAC 1579
QY 1501 AGACATGCTCCGACAGAGAGTGAACAGATCTGTTGAAATGAGAGAGGAATGAAAT 1560
DB 1580 AGACATGCTCCGACAGAGAGTGAACAGATCTGTTGAAATGAGAGAGGAATGAAAT 1639
QY 1561 AGGCAAGGAGCGCATGAGGACCTGCAAGGAGGCTGACATGAGTCACTTCCGACATCAT 1620
DB 1640 AGGCAAGGAGCGCATGAGGACCTGCAAGGAGGCTGACATGAGTCACTTCCGACATCAT 1699
QY 1621 CTCTTCCCTCTCCCATGATTTTGTTCCTTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 1680
DB 1700 CTCTTCCCTCTCCCATGATTTTGTTCCTTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 1759
QY 1681 GGCCTTGATTTAAAGGTTTGTGTCATTTCTTACAGATCTGGGTATGCTCACATGAGC 1740
DB 1760 GGCCTTGATTTAAAGGTTTGTGTCATTTCTTACAGATCTGGGTATGCTCACATGAGC 1819
QY 1741 GGGGAGCCTAGAGATGCTTTTACGTTGCTATGTTAAACAAACAAACAACTGACTT 1800
DB 1820 GGGGAGCCTAGAGATGCTTTTACGTTGCTATGTTAAACAAACAAACAACTGACTT 1879
QY 1801 CATACCCCTGCTCAGGAAACCCAAAGACAGAGTGGCTGACGTTGACGTTGCTC 1860

DB 1880 CATACCCCTGCTCAGGAAACCCAAAGACAGAGTGGCTGACGTTGACGTTGCTC 1939
QY 1861 TCTTCCCTGAGAAATCTCTCTTGGAAACCAAGACTGAGCTGTGGCATGGCGCTCG 1920
DB 1940 TCTTCCCTGAGAAATCTCTCTTGGAAACCAAGACTGAGCTGTGGCATGGCGCTCG 1999
QY 1921 GTCACTGTGACAGAGGACGACAGATCTCTCTGCTCCCTCTGATCCGCTTAAGAAATCA 1980
DB 2000 GTCACTGTGACAGAGGACGACAGATCTCTCTGCTCCCTCTGATCCGCTTAAGAAATCA 2059
QY 1981 CAGGTTAAACCTGAGCTTCTTGAATTTGCTTCCAGTCAATGAGCGGTCAAAAGATG 2040
DB 2060 CAGGTTAAACCTGAGCTTCTTGAATTTGCTTCCAGTCAATGAGCGGTCAAAAGATG 2119
QY 2041 GAGCCCGGCTGCTTAAATTTCCCTTCTGACAGAGTGTGAAACCATCTACTCCAC 2100
DB 2120 GAGCCCGGCTGCTTAAATTTCCCTTCTGACAGAGTGTGAAACCATCTACTCCAC 2179
QY 2101 ACATGAGAGAGGCGGTGACAGCTGACGCGGAGTCCCGCTTCACTGAGAGAACGA 2160
DB 2180 ACATGAGAGAGGCGGTGACAGCTGACGCGGAGTCCCGCTTCACTGAGAGAACGA 2239
QY 2161 GACTGTGACACAGAGCTGACAGATGACAGAAATCTCCGTAGAAAGTTGGTTTG 2220
DB 2240 GACTGTGACACAGAGCTGACAGATGACAGAAATCTCCGTAGAAAGTTGGTTTG 2299
QY 2221 AAATGCCCGGGGGGAGCAACAGATGAGTGAATGATGATGATTTCACTTGGCTTTC 2280
DB 2300 AAATGCCCGGGGGGAGCAACAGATGAGTGAATGATGATGATTTCACTTGGCTTTC 2359
QY 2281 CTAGATCTGAGCAAGCTGTCAGTTCACACCCCAACGCTATATACATGAGCAATCTT 2340
DB 2360 CTAGATCTGAGCAAGCTGTCAGTTCACACCCCAACGCTATATACATGAGCAATCTT 2419
QY 2341 TTAATTTGACAAAGGCGCATCTCCAGATTCAGACCTTGGCGATGACTTTTCTGAA 2400
DB 2420 TTAATTTGACAAAGGCGCATCTCCAGATTCAGACCTTGGCGATGACTTTTCTGAA 2479
QY 2401 GGGTGGCTTTTCCCTGCTTCTGAGAGTGGCATTAAGGAGTCAATGAGATTC 2460
DB 2480 GGGTGGCTTTTCCCTGCTTCTGAGAGTGGCATTAAGGAGTCAATGAGATTC 2539
QY 2461 TAACTTGAATTTTGTGTTTACAGTGAACAGTGAATTAAGTTCATCAAGATCTTA 2520
DB 2540 TAACTTGAATTTTGTGTTTACAGTGAACAGTGAATTAAGTTCATCAAGATCTTA 2599
QY 2521 TGCAGGTTGCTGAGGTTAACTTTTGAAGATTAATTAACCTGTTGCTATCTTA 2580
DB 2600 TGCAGGTTGCTGAGGTTAACTTTTGAAGATTAATTAACCTGTTGCTATCTTA 2659
QY 2581 GTCATPACTCTGCGGTGAACAGTGAATTAAGTGAATTAAGTGAATTAAGTGAATTAAGT 2640
DB 2660 GTCATPACTCTGCGGTGAACAGTGAATTAAGTGAATTAAGTGAATTAAGTGAATTAAGT 2719
QY 2641 AGCATTAAGCAAGATTTTATACGATACAGATCTATGAGTCTCTCCCTGAATA 2700
DB 2720 AGCATTAAGCAAGATTTTATACGATACAGATCTATGAGTCTCTCCCTGAATA 2779
QY 2701 AGCATTAAGCAAGATTTTATACGATACAGATTAATTTTGAAGTGAAGAGGTTT 2760
DB 2780 AGCATTAAGCAAGATTTTATACGATACAGATTAATTTTGAAGTGAAGAGGTTT 2839
QY 2761 CCTTTAAAGAAATTAAGACAGGTTTCAATTTGATTTATCGAATTTCTTAAGCTTA 2820
DB 2840 CCTTTAAAGAAATTAAGACAGGTTTCAATTTGATTTATCGAATTTCTTAAGCTTA 2899
QY 2821 AAGAACCTTAACAAAGAAATATTTAAGATTAATTAATATGCTATATGTTATCTAAT 2880
DB 2900 AAGAACCTTAACAAAGAAATATTTAAGATTAATTAATATGCTATATGTTATCTAAT 2959
QY 2881 TTAATTTGAGTATTAATTAATTTCTATTTTGGATTTTCAATTAATTAATTAATTAATTA 2940

Db 2960 TTATTTAGGCTAATAATCAATTCCTATTTCGATTTTCATTAATAATGCTTAATACA 3013

QY 2941 AAA 2943

Db 3020 ATA 3022

RESULT 4
LOCUS BC014526

DEFINITION Homo sapiens ankylosis, progressive homolog (mouse), mRNA (CDNA clone MGC:11142 IMAGE:3837372), complete cds.

ACCESSION BC014526

VERSION BC014526.2 GI:3878662

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 3013)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.U., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwen, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hult, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Schnerch, A., Schein, J.R., Jones, S.J., and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE 12477932

JOURNAL MEDLINE 22388257

REFERENCE 2 (bases 1 to 3013)
Strausberg, R.
Direct Submission
Submitted (24-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK

COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
On Aug 19, 2003 this sequence version replaced gi:15778895.
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed By: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadamsystemsbio.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting

FEATURES

SOURCE

Location/Qualifiers

1..3013

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/mol_type="mRNA"

/db_xref="taxon:9606"

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAL Plate: 14 Row: 9 Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21536393.

gene

1..3013

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/note="synonyms: ANK, HANK, MANK, CMDJ, CCAL2, CEPBD"

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/db_xref="GI:15778896"

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ORIGIN

Query Match 98.4%; Score 2896.8; DB 9; Length 3013;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2912; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

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1 CCGCAGAGTCCCTCCGCGGAGCAGCAGATGTGTGGGTGAGCCACGCGCGGGACCTATGG 60

QY 87 TGAATATCCCGCGGCTCAGCAGCAGTGTGCGCCGATCCGATCTTGTGTCCTCGGAGCA 146
Db 1 TGAATATCCCGCGGCTCAGCAGCAGTGTGCGCCGATCCGATCTTGTGTCCTCGGAGCA 120

QY 61 TGAATATCCCGCGGCTCAGCAGCAGTGTGCGCCGATCCGATCTTGTGTCCTCGGAGCA 120

Db 147 TCACCAATAGCCATGACCTGCGGGAGCAGGCGCTTGAACCGGGGACATGCTGCTGCA 206
121 TCACCAATAGCCATGACCTGCGGGAGCAGGCGCTTGAACCGGGGACATGCTGCTGCA 180

QY 207 AGAGAGATGAGTGAATGCTGCGCCAGCTGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 266
Db 181 AGAGAGATGAGTGAATGCTGCGCCAGCTGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 240

QY 267 TCACGGGTCCCATGAGTGAATGCTGCGCCAGCTGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 326
241 TCACGGGTCCCATGAGTGAATGCTGCGCCAGCTGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 300

QY 327 ACAGAGCAAAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 386
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Db 361 CACGTGATGCTTATAGTATGATTTAGATATCAATATCAATATCAATATCAATATCAATATCAAT 420

QY 447 AGTGGTGGGAGAGCAAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 506
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QY 507 ACCGATGAGATGAGACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 566
Db 481 ACCGATGAGATGAGACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540

QY 567 GATGTGCTCAATTCAGATGATCACTACAGTGTGTTGTCATTTGTCATTTGTCATTTGTCATTTGTCATTT 626
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